

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 12, 2003, 14:50:32 ; Search time 27 Seconds

(without alignments)
1215.103 Million cell updates/sec

Title: US-09-804-472-2

Perfect score: 4177

Sequence: 1 MDASSDPYLPYDGGGNIPL.....DILRHMAQTANODPASIMFN 791*

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3997	95.7	760	1	CLC3_CAVPO
2	3996	95.7	760	1	CLC3_MOUSE
3	3994	95.6	760	1	CLC3_RAT
4	3991	95.5	762	1	CLC3_HUMAN
5	3281	78.5	760	1	CLC4_HUMAN
6	3240	77.6	747	1	CLC4_RAT
7	3217	77.0	747	1	CLC4_MOUSE
8	3139.5	75.2	746	1	CLC5_HUMAN
9	3138.5	75.1	746	1	CLC5_RAT
10	3137.5	75.1	746	1	CLC5_MOUSE
11	996.5	23.9	779	1	GEET_YEAST
12	751	18.0	803	1	CLC7_MOUSE
13	751	18.0	803	1	CLC7_RAT
14	748.5	17.9	805	1	CLC7_HUMAN
15	725.5	17.4	869	1	CLC6_HUMAN
16	711	17.0	870	1	CLC6_MOUSE
17	658.5	15.8	902	1	CLC2_CAVPO
18	655.5	15.7	898	1	CLC2_HUMAN
19	652	15.6	907	1	CLC2_RAT
20	646	15.5	908	1	CLC2_MOUSE
21	637.5	15.3	908	1	CLC2_MOUSE
22	602.5	14.4	994	1	CLC1_RAT
23	594.5	14.2	994	1	CLC1_MOUSE
24	591	14.1	809	1	CLC1_TORCA
25	590.5	14.1	805	1	CLC1_TORNA
26	579.5	13.9	808	1	CLC1_HUMAN
27	536	12.8	687	1	CLC1_RABIT
28	530.5	12.7	687	1	CLC1_HUMAN
29	530	12.7	687	1	CLC1_HUMAN
30	528	12.6	687	1	CLC1_RAT
31	516	12.4	678	1	CLC1_RABIT
32	504.5	12.1	687	1	CLC1_RAT
33	342.5	8.2	468	1	ERIC_VIBCH

ALIGNMENTS

RESULT 1	ID	CLC3_CAVPO	STANDARD:	PRT:	760 AA.
AC	Q9R279;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Chloride channel protein 3 (CLC-3).				
GN	CLC3.				
OS	Cavia porcellus (Guinea pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.				
NCBI_TaxID=10141;					
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Small Intestine;				
RA	Varela D., Cid L.P., Sepulveda F.V.;				
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;				
CC	MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-TERM MEMORY (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.				
CC	-1- SIMILARITY: CONTAINS 2 CBS DOMAINS.				
CC	-----				
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CC	-----				
DR	EMBL: AF133214; ABD33599.1; -				
DR	InterPro: IPR001807; CL channel_volt.				
DR	InterPro: IPR001807; CL channel_volt.				
DR	Pfam: PF00571; CBS; 2.				
DR	Pfam: PF00654; Voltage_CLC; 1.				
DR	PRINTS: PR00762; CLCHANNEL.				
DR	SMART: SM00116; CBS; 2.				
KW	Ionic channel; Ion transport; Voltage-gated channel; Transmembrane; CBS domain; Repeat.				
FT	TRANSMEM 68				POTENTIAL.
FT	TRANSMEM 154				POTENTIAL.
FT	TRANSMEM 175				POTENTIAL.
FT	TRANSMEM 195				POTENTIAL.
FT	TRANSMEM 202				POTENTIAL.
FT	TRANSMEM 222				POTENTIAL.
FT	TRANSMEM 259				POTENTIAL.
FT	TRANSMEM 279				POTENTIAL.
FT	TRANSMEM 285				POTENTIAL.
FT	TRANSMEM 305				POTENTIAL.
FT	TRANSMEM 330				POTENTIAL.
FT	TRANSMEM 350				POTENTIAL.
FT	TRANSMEM 365				POTENTIAL.
FT	TRANSMEM 442				POTENTIAL.
FT	TRANSMEM 462				POTENTIAL.
FT	TRANSMEM 467				POTENTIAL.
FT	TRANSMEM 487				POTENTIAL.

34	304.5	7.3	473	1	ERIC_SALTI	0829b3 salmonella
35	304.5	7.3	473	1	ERIC_SALTY	0829b8 salmonella
36	294.5	7.1	478	1	ERIC_YERPE	082bno yersinia pe
37	284.5	6.8	473	1	ERIC_ECOLI	p37019 escherichia
38	283.5	6.8	473	1	ERIC_ECO57	p58244 escherichia
39	260.5	6.2	461	1	ERIC_RALSO	08xt4 ralsostonia s
40	235	5.6	430	1	ERIC_YERPE	082eb3 yersinia pe
41	230	5.5	429	1	ERIC_YERPS	09agq5 yersinia ps
42	227.5	5.4	395	1	Y305_MENJA	057753 methanococ
43	208	5.0	438	1	ERIC_ECO57	08x794 escherichia
44	208	5.0	438	1	ERIC_ECOLI	p76175 escherichia
45	205	4.9	437	1	ERIC_SALTI	0826y0 salmonella

FT TRANSMEM 508 528 POTENTIAL.
 FT TRANSMEM 536 556 POTENTIAL.
 FT DOMAIN 599 659 CBS 1.
 FT DOMAIN 696 747 CBS 2.
 SQ SEQUENCE 760 AA: 84485 MM: BC2E2A5BE60B3D CRC64:

Query Match 95.7%; Score 3997; DB 1; Length 760;
 Best local Similarity 99.7%; Pred. No. 2.5e-278;
 Matches 758; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 32 MTNGSGINSSHHLLDLDDEPIPGYVDDEFTIDWREKCKDRRRHRINSKKESAMEM 91
 DB 1 MTNGSGINSSHHLLDLDDEPIPGYVDDEFTIDWREKCKDRRRHRINSKKESAMEM 60
 QY 92 TKSLYDAMSGMLVYTLTGLASGALAGLIDADMMTDLKEGICLSALMYNEOCCWSNE 151
 DB 61 TKSLYDAMSGMLVYTLTGLASGALAGLIDADMMTDLKEGICLSALMYNEOCCWSNE 120
 QY 152 TTEPERKCPQWKTWABLLIGQAECPQSYIMNYTFWALSFAFLAVSLVKVAPYACG 211
 DB 121 TTEPERKCPQWKTWABLLIGQAECPQSYIMNYTFWALSFAFLAVSLVKVAPYACG 180
 QY 212 SGPEITILISGFIIRGLKWTIMKITTLVLAASGLSGKEGPLVHVACCCGNFSY 271
 DB 181 SGPEITILISGFIIRGLKWTIMKITTLVLAASGLSGKEGPLVHVACCCGNFSY 240
 QY 272 LEPYSTNEAKKREVLNANASAGVAFGAPIGGVLSLEEVSYFPLKTLMSFFALV 331
 DB 241 LEPYSTNEAKKREVLNANASAGVAFGAPIGGVLSLEEVSYFPLKTLMSFFALV 300
 QY 332 AAFVLRISINPFGNSRLVFEYEHYHTPWYLFELFPFILLGVFGIGMAFFIRANTAMCRR 391
 DB 301 AAFVLRISINPFGNSRLVFEYEHYHTPWYLFELFPFILLGVFGIGMAFFIRANTAMCRR 360
 QY 392 KSTFEGYPLEVETIYAVIAFVAFNPYPTLNTSELKEFTFCGPLESSLCDYRNDM 451
 DB 361 KSTFEGYPLEVETIYAVIAFVAFNPYPTLNTSELKEFTFCGPLESSLCDYRNDM 420
 QY 452 NASKIVDIDPRPAGISGVSAIMOLCLALFKIMTVEFTGIRKPSGLTIPSAIGAAG 511
 DB 421 NASKIVDIDPRPAGISGVSAIMOLCLALFKIMTVEFTGIRKPSGLTIPSAIGAAG 480
 QY 512 RIVGIANEOLAYYHHMFIFIREKCEVACDCTTPEGLYANVGAACLGVTTRMTVSLVIVF 571
 DB 481 RIVGIANEOLAYYHHMFIFIREKCEVACDCTTPEGLYANVGAACLGVTTRMTVSLVIVF 540
 QY 572 ELTGLGLYIYPLMAAVMTSKVGDFAFREGIYEAHIRLNGPFLDAKEEFHTTLADVM 631
 DB 541 ELTGLGLYIYPLMAAVMTSKVGDFAFREGIYEAHIRLNGPFLDAKEEFHTTLADVM 600
 QY 632 RPRRNDPPLAVLTQDNMTVDIDEMKINETSNGFPVIMSKESQRLVGFALRDLJTIAES 691
 DB 601 RPRRNDPPLAVLTQDNMTVDIDEMKINETSNGFPVIMSKESQRLVGFALRDLJTIAES 660
 QY 692 ARKQEBIVSSSRKCFQHPHPSLPAESPRPLKSLIIDSMSFTYTDHTPMETIVDIRKL 751
 DB 661 ARKQEBIVSSSRKCFQHPHPSLPAESPRPLKSLIIDSMSFTYTDHTPMETIVDIRKL 720
 QY 752 GLRQCLVTHNGRLGLITTKKDIERHMAQTANODPASIMFN 791
 DB 721 GLRQCLVTHNGRLGLITTKKDIERHMAQTANODPASIMFN 760

RESULT 2
 CLC3 MOUSE
 ID CLC3 MOUSE STANDARD; PRT; 760 AA.

AC P51791;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chloride channel protein 3 (CLC-3).
 GN CLC3 OR CLC3.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RX MEDLINE=95394449; PubMed=7665160;
 RA Borsani G., Rugaili E.I., Taglialatela M., Wong C., Ballabio A.;
 RT "Characterization of a human and murine gene (CLC3) sharing
 RT similarities to voltage-gated chloride channels and to a yeast
 RT integral membrane protein.";
 RL Genomics 27:131-141(1995).
 CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
 CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
 CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
 CC TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL
 CC CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY
 CC PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-
 CC TERM MEMORY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE KIDNEY WHILE A
 CC LOW LEVEL EXPRESSION IS SEEN IN THE BRAIN. WITHIN THE BRAIN, IT IS
 CC PROMINENT IN THE HIPPOCAMPUS, CEREBRAL CORTEX AND OLFACTORY BULB.
 CC -1- DEVELOPMENTAL STAGE: AT 10.5 DAYS OF DEVELOPMENT IT IS EXPRESSED
 CC THROUGHOUT THE EMBRYO. LATER IN DEVELOPMENT (12.5 TO 14.5 DAYS OF
 CC GESTATION), EXPRESSION IS PROGRESSIVELY UPREGULATED IN NEURONS OF
 CC THE BRAIN AND THE SPINAL CORD, IN ALL CRANIAL SENSORY GANGLIA AND
 CC IN THE SYMPATHETIC DORSAL ROOT GANGLIA.
 CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC -----
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 CC -----
 DR EMBL: X78874; CA55476.1; -
 DR MGD: MG1:103555; Clcn3.
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR001807; Cl-channel_volt.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00654; voltage_CLC; 1.
 DR PRINTS: PR00762; CLCHANNEL.
 DR SMART: SM00116; CBS; 2.
 KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
 KW CBS domain; Repeat.
 FT TRANSMEM 68 88 POTENTIAL.
 FT TRANSMEM 154 174 POTENTIAL.
 FT TRANSMEM 175 195 POTENTIAL.
 FT TRANSMEM 202 222 POTENTIAL.
 FT TRANSMEM 259 279 POTENTIAL.
 FT TRANSMEM 285 305 POTENTIAL.
 FT TRANSMEM 330 350 POTENTIAL.
 FT TRANSMEM 365 385 POTENTIAL.
 FT TRANSMEM 442 462 POTENTIAL.
 FT TRANSMEM 467 487 POTENTIAL.
 FT TRANSMEM 508 528 POTENTIAL.
 FT TRANSMEM 536 556 POTENTIAL.
 FT TRANSMEM 599 659 CBS 1.
 FT DOMAIN 696 747 CBS 2.
 FT VARIANT 653 653 D -> N.
 FT VARIAT 653 653
 SQ SEQUENCE 760 AA: 84475 MM: 0101C45A23509AFE CRC64:

Query Match 95.7%; Score 3996; DB 1; Length 760;
 Best local Similarity 99.7%; Pred. No. 3e-278;
 Matches 758; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 32 MTNGSGINSSHHLLDLDDEPIPGYVDDEFTIDWREKCKDRRRHRINSKKESAMEM 91
 DB 1 MTNGSGINSSHHLLDLDDEPIPGYVDDEFTIDWREKCKDRRRHRINSKKESAMEM 60

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QY 92 TKSLYDAMSGMLVYVLTGLASGALAGLIDIAADWMTDKEGICISALWYNHDOCCWGSNE 151
D 61 TKSLYDAMSGMLVYVLTGLASGALAGLIDIAADWMTDKEGICISALWYNHDOCCWGSNE 120
QY 152 TTFEERDKCPQWKWAEIITGOABEGPSYIMNYIMYIFWALSFAFLAVSLKVPAPYACG 211
D 121 TTFEERDKCPQWKWAEIITGOABEGPSYIMNYIMYIFWALSFAFLAVSLKVPAPYACG 180
QY 212 SGIPFIKTIISGFIIRGLGKWTLMIKITITLVAVASGLSGKEBPLVHVACCCGNIIFY 271
D 181 SGIPFIKTIISGFIIRGLGKWTLMIKITITLVAVASGLSGKEBPLVHVACCCGNIIFY 240
QY 272 LFPKSTNEAKKREVLASAASAGSVAFAGPIGVLFSLSEYSYFFPLKTIWRSFFALV 331
D 241 LFPKSTNEAKKREVLASAASAGSVAFAGPIGVLFSLSEYSYFFPLKTIWRSFFALV 300
QY 332 AAFVYLRSTNPGNSRLVLYFEYEHRTWYLFELFPFILLGVFGMLGAFPIRANIAMCRRR 391
D 301 AAFVYLRSTNPGNSRLVLYFEYEHRTWYLFELFPFILLGVFGMLGAFPIRANIAMCRRR 360
QY 392 KSTRKGKXPVLEVIIVATVIAFPNPTRLNSELKELFTDCGPLSSSLCDYRDM 451
D 361 KSTRKGKXPVLEVIIVATVIAFPNPTRLNSELKELFTDCGPLSSSLCDYRDM 420
QY 452 NASKIVDDIPDRPAGIGVYSAIMQCLALFKIIMTVFTFGIKVPSGLFIPSMAGIAG 511
D 421 NASKIVDDIPDRPAGIGVYSAIMQCLALFKIIMTVFTFGIKVPSGLFIPSMAGIAG 480
QY 512 RIVGIVAGQALYYHHDMFIFEKCEVAGDCITPGLIYAVGAACIGVTRMTVSLVIVF 571
D 481 RIVGIVAGQALYYHHDMFIFEKCEVAGDCITPGLIYAVGAACIGVTRMTVSLVIVF 540
QY 572 ELTGGLXIVPLMAAVMSKMWGDAFREGIYEAHIRLNGYPLIDAKKEFHTTLAAVYM 631
D 541 ELTGGLXIVPLMAAVMSKMWGDAFREGIYEAHIRLNGYPLIDAKKEFHTTLAAVYM 600
QY 632 RPRNDPELAVLTODNMVVDIENMINETSYNGFPVIMSKESQRLVGFALRRDLTIAES 691
D 601 RPRNDPELAVLTODNMVVDIENMINETSYNGFPVIMSKESQRLVGFALRRDLTIAES 660
QY 692 ARKKEGIVGSSRCFAOHTPSLPAESPRPLKLSILDMSEPTVTDHTPMEIIVDIEFKL 751
D 661 ARKKEGIVGSSRCFAOHTPSLPAESPRPLKLSILDMSEPTVTDHTPMEIIVDIEFKL 720
QY 752 GLROCLVTHNGRLGLITTKDILRHMAOTANODPASIMFN 791
D 721 GLROCLVTHNGRLGLITTKDILRHMAOTANODPASIMFN 760

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CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL
CC CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY
CC PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-
CC TERM MEMORY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, ESPECIALLY IN THE OLFACTORY
CC BULB, HIPPOCAMPUS, AND CEREBELLUM. A MODERATE EXPRESSION IS SEEN
CC IN THE LUNG, KIDNEY AND ADRENAL GLAND.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC
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CC
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CC EMBL: D17521; BAA04471.1; -.
CC InterPro: IPR000644; CBS_domain.
CC InterPro: IPR001807; Cl-channel_volt.
CC Pfam: PF00571; CBS; 2.
CC Pfam: PF00654; voltage_CLC; 1.
CC DR PRINTS: PR00762; CLCHANNEL.
CC SMART: SM00116; CBS; 2.
CC
CC Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
CC CBS domain; Repeat.
CC FT TRANSSEM 68 88 POTENTIAL.
CC FT TRANSSEM 154 174 POTENTIAL.
CC FT TRANSSEM 175 195 POTENTIAL.
CC FT TRANSSEM 202 222 POTENTIAL.
CC FT TRANSSEM 259 279 POTENTIAL.
CC FT TRANSSEM 285 305 POTENTIAL.
CC FT TRANSSEM 330 350 POTENTIAL.
CC FT TRANSSEM 365 385 POTENTIAL.
CC FT TRANSSEM 442 462 POTENTIAL.
CC FT TRANSSEM 467 487 POTENTIAL.
CC FT TRANSSEM 508 528 POTENTIAL.
CC FT TRANSSEM 536 556 POTENTIAL.
CC FT DOMAIN 599 659 CBS 1.
CC FT DOMAIN 696 747 CBS 2.
CC SO SEQUENCE 760 AA; 84447 MW; 8A826FCA2497269C CMC64;

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Query Match 95.6%; Score 3994; DB 1; Length 760;
Best Local Similarity 99.5%; Pred. No. 4,le-278;
Matches 756; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 32 MTNGSTNSSTHILDLDEPIGVGTVDPTHTIDVREKCKDREHRRIRNSKKKESAMEM 91
D 1 MTNGSTNSSTHILDLDEPIGVGTVDPTHTIDVREKCKDREHRRIRNSKKKESAMEM 60
QY 92 TKSLYDAMSGMLVYVLTGLASGALAGLIDIAADWMTDKEGICISALWYNHDOCCWGSNE 151
D 61 TKSLYDAMSGMLVYVLTGLASGALAGLIDIAADWMTDKEGICISALWYNHDOCCWGSNE 120
QY 152 TTFEERDKCPQWKWAEIITGOABEGPSYIMNYIMYIFWALSFAFLAVSLKVPAPYACG 211
D 121 TTFEERDKCPQWKWAEIITGOABEGPSYIMNYIMYIFWALSFAFLAVSLKVPAPYACG 180
QY 212 SGIPFIKTIISGFIIRGLGKWTLMIKITITLVAVASGLSGKEBPLVHVACCCGNIIFY 271
D 181 SGIPFIKTIISGFIIRGLGKWTLMIKITITLVAVASGLSGKEBPLVHVACCCGNIIFY 240
QY 272 LFPKSTNEAKKREVLASAASAGSVAFAGPIGVLFSLSEYSYFFPLKTIWRSFFALV 331
D 241 LFPKSTNEAKKREVLASAASAGSVAFAGPIGVLFSLSEYSYFFPLKTIWRSFFALV 300
QY 332 AAFVYLRSTNPGNSRLVLYFEYEHRTWYLFELFPFILLGVFGMLGAFPIRANIAMCRRR 391
D 301 AAFVYLRSTNPGNSRLVLYFEYEHRTWYLFELFPFILLGVFGMLGAFPIRANIAMCRRR 360

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QY	392	KSTFGKPVLEVTIVAAITAVIAFVAFVPPVYRRLNLTSELIKELFTDCGPLESSSLCYDRNDM	451
QY	392	KSTFGKPVLEVTIVAAITAVIAFVAFVPPVYRRLNLTSELIKELFTDCGPLESSSLCYDRNDM	451
Db	361	KSTFGKPVLEVTIVAAITAVIAFVAFVPPVYRRLNLTSELIKELFTDCGPLESSSLCYDRNDM	420
QY	452	NASKIVDDIPDRPAGIGVSAIMOLCLALIFKIMTFVFFGIVKVPSCGLFIPSMAGIAG	511
Db	421	NASKIVDDIPDRPAGIGVSAIMOLCLALIFKIMTFVFFGIVKVPSCGLFIPSMAGIAG	480
QY	512	RIVGAVBOLAAVYHHDMFIFREKCEVGCADITGGLVAMGAACLGAVRMVSLVIVF	571
Db	481	RIVGAVBOLAAVYHHDMFIFREKCEVGCADITGGLVAMGAACLGAVRMVSLVIVF	540
QY	572	ELTGGLEIYVPLMAAVNTSKWVGDAFREGIEYAHIRKLVNGVLPFLDAKEEFTHTTLAADVW	631
Db	541	ELTGGLEIYVPLMAAVNTSKWVGDAFREGIEYAHIRKLVNGVLPFLDAKEEFTHTTLAADVW	600
QY	632	RPRRNDPPLAVLTODNMTVDDIENMIMETSYNGFPVIMSKESQRLVGFAIRDLDTIAIES	691
Db	601	RPRRNDPPLAVLTODNMTVDDIENMIMETSYNGFPVIMSKESQRLVGFAIRDLDTIAIES	660
QY	692	ARKKQEGVSSRCFCFQHPSPSPAESPRPLKRLSLIDMSPFVDTHTMETVVDVFRKL	751
Db	661	ARKKQEGVSSRCFCFQHPSPSPAESPRPLKRLSLIDMSPFVDTHTMETVVDVFRKL	720
QY	752	GLRCLVTHNGRLIGITTKRDILRHMAQTANODPASIMFN	791
Db	721	GLRCLVTHNGRLIGITTKRDILRHMAQTANODPASIMFN	760
RESULT 4			
CLC3_HUMAN			
ID	CLC3_HUMAN	STANDARD;	PRT; 762 AA.
AC	PS1790;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Chloride channel protein 3 (CLC-3).		
GN	CLCN3.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Retina;		
RX	MEDLINE=95394449; PubMed=7665160;		
RA	Borsani G., Rugaili E.I., Tgallalabela M., Wong C., Ballabio A.;		
RT	"Characterization of a human and murine gene (CLCN3) sharing		
RT	similarities to voltage-gated chloride channels and to a yeast		
RT	integral membrane protein.";		
RL	Genomics 27:131-141(1995).		
RN	[2]		
RP	TISSUE SPECIFICITY.		
RC	TISSUE=vascular smooth muscle, Aortic endothelium, and Fetal lung;		
RX	MEDLINE=99222497; PubMed=10198195;		
RA	Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,		
RT	Schutte B.C.;		
RT	"Expression of CLCN voltage-gated chloride channel genes in human		
RT	blood vessels.";		
RL	J. Mol. Cell. Cardiol. 31:657-666(1999).		
CC	-1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE		
CC	SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;		
CC	MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND		
CC	TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL		
CC	CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY		
CC	PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT		
CC	TERM MEMORY.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN TISSUES DERIVED FROM		
CC	NEUROECODERM. WITHIN THE BRAIN, ITS EXPRESSION IS PARTICULARLY		
CC	EVIDENT IN THE HIPPOCAMPUS, OLFACTORY CORTEX, AND OLFACTORY BULB.		
CC	HIGHLY EXPRESSED IN AORTIC AND CORONARY VASCULAR SMOOTH MUSCLE		

CC	CELLS, AND AORTIC ENDOTHELIAL CELLS. ALSO EXPRESSED IN THYCAEAL
CC	AND ALVEOLAR EPITHELIAL CELLS, AND INTIMA AND MEDIA OF THE
CC	PULMONARY VESSELS.
CC	-1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC	-1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC	-----
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CC	entities requires a license agreement (see http://www.isb-sb.ch/announce/
CC	or send an email to license@isb-sb.ch).
CC	-----
DR	EMBL: X78520; CAA55280.1; -
DR	EMBL: X78520; CAA55280.1; ALT_INIT.
DR	Genew: HGNC:2021; CLCN3.
DR	MIM: 600580; -
DR	InterPro: IPR000644; CBS_domain.
DR	InterPro: IPR001807; C1-channel_volt.
DR	Pfam: PF00571; CBS; 2.
DR	Pfam: PF00654; voltage_CLC; 1.
DR	PRINTS: PR00762; CLCHANNEL.
DR	SMART: SM00116; CBS; 2.
KW	Ionic channel; Ion transport; voltage-gated channel; Transmembrane;
KW	CBS domain; Repeat.
FT	TRANSMEM 68 88 POTENTIAL.
FT	TRANSMEM 154 174 POTENTIAL.
FT	TRANSMEM 175 195 POTENTIAL.
FT	TRANSMEM 202 222 POTENTIAL.
FT	TRANSMEM 259 279 POTENTIAL.
FT	TRANSMEM 285 305 POTENTIAL.
FT	TRANSMEM 330 350 POTENTIAL.
FT	TRANSMEM 365 385 POTENTIAL.
FT	TRANSMEM 442 462 POTENTIAL.
FT	TRANSMEM 467 487 POTENTIAL.
FT	TRANSMEM 508 528 POTENTIAL.
FT	TRANSMEM 536 556 POTENTIAL.
FT	DOMAIN 577 616 CBS 1.
FT	DOMAIN 698 749 CBS 2.
SO	SEQUENCE 762 AA; 84792 MW; 8FC0F0E132001B9C0 CRC64;
Query Match	95.5%; Score 3991; DB 1; Length 762;
Best Local Similarity	99.7%; Pred. No. 6.8e-278;
Matches 760; Conservative 0; Mismatches 0; Indels 2; Gaps 1	
QY 32	MTNGGSISSHTLDDLPDEIPGVGTDFHTIDVWRREKCKDREHRRIRNSKKKSASWEM 91
DB 1	MENGGSISSHTLDDLPDEIPGVGTDFHTIDVWRREKCKDREHRRIRNSKKKSASWEM 60
QY 92	TKSLYDANSGMLVYLTGLASGALAGLIDIANDMWTDLKEGICLSALWYNEHQCCKSNE 151
DB 61	TKSLYDANSGMLVYLTGLASGALAGLIDIANDMWTDLKEGICLSALWYNEHQCCKSNE 120
QY 152	TTFERDCKCPQKWTAEELITGOAEGPSGSIYMYIMYIFWALSFAFLAVSLVVPAPYACG 211
DB 121	TTFERDCKCPQKWTAEELITGOAEGPSGSIYMYIMYIFWALSFAFLAVSLVVPAPYACG 180
QY 212	SGIPEIKITLSGFIIRGYLGKWTLMIKITTVLAVASGLSLGKEGSPVLVHACCCGNTFSY 271
DB 181	SGIPEIKITLSGFIIRGYLGKWTLMIKITTVLAVASGLSLGKEGSPVLVHACCCGNTFSY 240
QY 272	LEPKSTTEAKRKREVLASASAGSVAGAPIGVGLFSLEEVSYFPLKTIWRSEFAALY 331
DB 241	LEPKSTTEAKRKREVLASASAGSVAGAPIGVGLFSLEEVSYFPLKTIWRSEFAALY 300
QY 332	AAFLVRSINPEKNSRLVFEYVEHTPWVLFELFPIILLGVDFQGLMGAFPIRANIAMCRR 391
DB 301	AAFLVRSINPEKNSRLVFEYVEHTPWVLFELFPIILLGVDFQGLMGAFPIRANIAMCRR 360
QY 392	KSTFGKPLVLEVIIVAAITAVIAFPNPTYRLNLSLIKELFTDCGPLESSSLCQYRDM 451
DB 361	KSTFGKPLVLEVIIVAAITAVIAFPNPTYRLNLSLIKELFTDCGPLESSSLCQYRDM 420

OY 452 NSKIVDDIPDRPAGIGVSAIMQCLALFKIIMTVTFEGIKVPSGLFIPSAIGAIA 511
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 421 NSKIVDDIPDRPAGIGVSAIMQCLALFKIIMTVTFEGIKVPSGLFIPSAIGAIA 480
 OY 512 RIYGIAYEQLAYHHHMFWEFFKEWCEVAGADCIPTGLYAMGAACLGIVRMVSLVYIV 511
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 481 RIYGIAYEQLAYHHHMFWEFFKEWCEVAGADCIPTGLYAMGAACLGIVRMVSLVYIV 540
 OY 572 ELTGLEYIVPLMAAVMTSKWGDAGRGIEYEAHRLNGYPLDLAKE--EEFHTLAD 629
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 541 ELTGLEYIVPLMAAVMTSKWGDAGRGIEYEAHRLNGYPLDLAKEEEFHTLAD 600
 OY 630 VMRRNDPPLAVLTODNMTVDDIEMNINETSNGFPVIMSKESQRLVGFALRDLTIAI 689
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 601 VMRRNDPPLAVLTODNMTVDDIEMNINETSNGFPVIMSKESQRLVGFALRDLTIAI 660
 OY 690 ESARKKQEGIVSSRVCFOHPTSPALPESPRPLKRSIIDMSFFVTYDHTPMEIVDIFR 749
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 661 ESARKKQEGIVSSRVCFOHPTSPALPESPRPLKRSIIDMSFFVTYDHTPMEIVDIFR 720
 OY 750 KIGLRQCLVTHNGRLGIIITTKKDIILRHMAQTANQDPASIMFN 791
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 721 KIGLRQCLVTHNGRLGIIITTKKDIILRHMAQTANQDPASIMFN 762
 RESULT 5
 CLC4_HUMAN STANDARD: PRT: 760 AA.
 AC P51793; Q9UBU1; Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chloride channel protein 4 (CLC-4).
 GN CLC4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP TISSUE=Retina.
 RC TISSUE=Retina.
 RX MEDLINE=94348498; PubMed=8069296;
 RA van Slegtenhorst M.A., Bassi M.T., Borsani G., Wapenaar M.C.,
 RA Ferrero G.B., de Conchillos L., Ruggeri E.I., Grillo A., Franco B.,
 RA Zoghbi H.Y., Ballabio A.;
 RT "A gene from the Xp22.3 region shares homology with voltage-gated
 RT chloride channels";
 RL Hum. Mol. Genet. 3:547-552(1994).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=20035030; PubMed=10564087;
 RA Kawasaki M., Fukuma T., Yamauchi K., Sakamoto H., Marumo F.,
 RA Sasaki S.;
 RT "Identification of an acid-activated Cl- channel from human skeletal
 RT muscle";
 RL Am. J. Physiol. 277:C948-C954(1999).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lens epithelium;
 RA Rae J.L.;
 RT "A chloride channel (CLC-4) in human lens epithelium";
 RT Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
 CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
 CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
 CC TRANSEPITHELIAL TRANSPORT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN SKELETAL MUSCLE AND ALSO
 CC DETECTABLE IN BRAIN AND HEART.
 CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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 CC -----
 CC EMBL: X77197; CA54417.1; -
 CC EMBL: AB019432; BA477327.1; -
 CC EMBL: AF170492; AAD50981.1; -
 CC Genew: HGNC:2022; CLC4.
 CC MIM: 302910; -
 CC InterPro: IPR006644; CBS domain.
 CC InterPro: IPR001807; Cl-channel_volt.
 CC Pfam: PF00654; voltage_CLC; 1.
 CC Pfam: PF00762; CLCHANNEL.
 CC SMART: SM00116; CBS; 2.
 CC K1 Ion channel; Ion transport; Voltage-gated channel; Transmembrane;
 CC K1 CBS domain; Repeat.
 CC FT TRANSMEM 66 88 POTENTIAL.
 CC FT TRANSMEM 148 168 POTENTIAL.
 CC FT TRANSMEM 202 222 POTENTIAL.
 CC FT TRANSMEM 259 279 POTENTIAL.
 CC FT TRANSMEM 330 350 POTENTIAL.
 CC FT TRANSMEM 365 385 POTENTIAL.
 CC FT TRANSMEM 442 462 POTENTIAL.
 CC FT TRANSMEM 467 487 POTENTIAL.
 CC FT TRANSMEM 508 528 POTENTIAL.
 CC FT TRANSMEM 535 555 POTENTIAL.
 CC FT DOMAIN 599 659 CBS 1.
 CC FT DOMAIN 697 747 CBS 2.
 CC FT CONFLICT 178 178 A -> R (IN REF. 1).
 CC FT CONFLICT 498 499 II -> YY (IN REF. 1).
 CC FT CONFLICT 659 659 K -> N (IN REF. 1).
 CC SQ SEQUENCE 760 AA: 84916 MW: 345425D1FEF3F217 CRC64;
 Query Match 78.5%; Score 3281; DB:1; Length 760;
 Best Local Similarity 78.2%; Pred. No. 4,2e-227;
 Matches 594; Conservative 83; Mismatches 83; Indels 0; Gaps 0;
 OY 32 MTNGSGINSTHLLDLEDPVGTDPHTIDWYREKCKDERRRRIRSKKESAMEM 91
 DB 1 MVAAGAMSGSGLNDPLDEFPVGYEDPHTIDWYREKCKDERRRRIRSKKESAMEM 60
 OY 92 TNSLYDAMSGWLVTLTGLASGALGLIDIDADMWDLREGICLSALMYNHQCCWGSNE 151
 DB 61 IKSILDAMSGWVYMLLIGLAGTLAGVIDLAVDMWDLREGVCLSAFWYSHQCCWTSNE 120
 OY 152 TTFEEDKCPOMKTMALIIIGQAGPGSYIMNYIMYIFALSAFLAVSYKFAFAYACG 211
 DB 121 TTFEEDKCPOMKTMALIIIGQAGPGSYIMNYIMYIFALSAFLAVSYKFAFAYACG 180
 OY 212 SGPEIKTILSGFTIRGYLGKMTIKITTLVAVASGLSKEGDLVHVAACCGNIFY 271
 DB 181 SGPEIKTILSGFTIRGYLGKMTIKITTLVAVASGLSKEGDLVHVAACCGNIFY 240
 OY 272 LPPKYSTNEAKKREVLSAASAGVSAFAPIGVLFSLSEVSYRPLKTLWRSFAALV 331
 DB 241 LPPKYSTNEAKKREVLSAASAGVSAFAPIGVLFSLSEVSYRPLKTLWRSFAALV 300
 OY 332 AAFVLSINPFGSRLVLEVEYHTPWYLFELFPFTLLGVFGILKMAFFRAIACRRR 391
 DB 301 AAFVLSINPFGSRLVLEVEYHTPWYLFELFPFTLLGVFGILKMAFFRAIACRRR 360
 OY 392 KSTKFGKRVLEVIYAATAVIAFPNPTRLNLSLIELFDDCPLESSSLCDVRNDM 451
 DB 361 KSTKFGKRVLEVIYAATAVIAFPNPTRLNLSLIELFDDCPLESSSLCDVRNDM 420
 OY 452 NSKIVDDIPDRPAGIGVSAIMQCLALFKIIMTVTFEGIKVPSGLFIPSAIGAIA 511
 DB 421 NSKIVDDIPDRPAGIGVSAIMQCLALFKIIMTVTFEGIKVPSGLFIPSAIGAIA 480

```

Db 421 NMTRPVDDIPDRPAGVGYTAMQALALJFKIVITJTEGSMKIPSGLEIPSMAGVAGIAG 480
Oy 512 RIVGIAVEOLAYYHHDFEFKEMCEVADCTTGLYAMVGAACLGTVTRMVSUVIYVE 571
Db 481 RMVIGIEVOLAYHHHDMIIIFRNMCPRGADCTPGLYAMVGAACLGTVTRMVSUVIYVE 540
Oy 572 ELTNGLEYVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPPILDAAEEFTHTTLADVM 631
Db 541 ELTNGLEYVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPPILDAAEEFTHTTLADVM 600
Oy 632 RPRRNDPPLAVLNDQNMVDDIEMNINETSNGFPVIMSKSQRSLVGPALPRDLTIAES 691
Db 601 RPRRNDPPLAVLNDQNMVDDIEMNINETSNGFPVIMSKSQRSLVGPALPRDLTIAES 660
Oy 692 ARKROEGIVSSRVCFAQHPPSLPAESPRLKLSILDMSPFTVTDHTPMEIYVDFEKL 751
Db 661 ARKROEGIVSSRVCFAQHPPSLPAESPRLKLSILDMSPFTVTDHTPMEIYVDFEKL 720
Oy 752 GLRQCLVTHNGRLGIIITKKDILRHMAOTANODPASTIMFN 791
Db 721 GLRQCLVTHNGRLGIIITKKDILRHMAOTANODPASTIMFN 760

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RESULT 6
CLC4_RAT
ID CLC4_RAT STANDARD: PRT: 747 AA.
AC P51794;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 4 (CLC-4).
GN CLC4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=95248463; Pubmed=7730971;
RA Jentsch T.J., Guenther M., Pusch M., Schwappach B.;
RT "Properties of voltage-gated chloride channels of the CLC gene
RT family."
RL J. Physiol. (Lond) 482:19-25(1995).
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LIVER AND BRAIN, BUT
CC ALSO IN HEART, MUSCLE, KIDNEY AND SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL: Z36944; CAAB5406.1; -
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; CL-channel_volt.
DR Pfam: PF00571; CBS_2.
DR Pfam: PF00654; voltage_CLC_1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain; Repeat.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 135 155 POTENTIAL.
FT TRANSMEM 189 209 POTENTIAL.

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FT TRANSMEM 246 266 POTENTIAL.
FT TRANSMEM 317 337 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 429 449 POTENTIAL.
FT TRANSMEM 454 474 POTENTIAL.
FT TRANSMEM 495 515 POTENTIAL.
FT TRANSMEM 522 542 POTENTIAL.
FT DOMAIN 586 646 CBS 1.
FT DOMAIN 684 734 CBS 2.
SQ SEQUENCE 747 AA; 83701 MW; E86B5732248BA0C3 CRC64;

Query Match 77.6% Score 3240; DB 1: Length 747;
Best Local Similarity 78.4% Pred. No. 3,5e-224;
Matches 586; Conservative 81; Mismatches 80; Indels 0; Gaps 0;

Oy 45 LDLDPEIPGYGDDPFTTIDMREKCDRERHRIRNSKKKSEAWEMTKSLYDAMSGVLY 104
Db 1 MDLDEPPDYGYEDRHTIDMLREKSRDIDRHKRTSKSKESIWEPIKSLIDAMSGVLY 60
Oy 105 VLTGLASGALAGLIDIAADMMTDLKEGICLSALVNHEDCCMGSNETTPEERDKCPQK 164
Db 61 MLLIGLAGTAGVIDLAVDMMDLKEGVCLSAFWYSHQCCWTSNETTFEDRDKCPQK 120
Oy 165 TWAEIIQOABPGSGYIMNYIMYIFWALSTFAFLAVSLKVPAPYACSGIPEITILSGF 224
Db 121 KWSELLLSQSEGSAGAYILNMYIMYIMALLFAFLAVSLVRFAPYACSGIPEITILSGF 180
Oy 225 IIRYGLKWTMLKITTLVLAVASGLSGKRGPIVHVACCGNIFSYLPYSTNEAKKR 284
Db 181 IIRYGLKWTMLKITTLVLAVASGLSGKRGPIVHVACCGNIFSYLPYSTNEAKKR 240
Oy 285 EVLSAASAGYVAFGAPIGGLVLSLEEVSYFPPLKTLMSRFALVAFLVRSINFGN 344
Db 241 EVLSAASAGYVAFGAPIGGLVLSLEEVSYFPPLKTLMSRFALVAFLVRSINFGN 300
Oy 345 SRLVFEYEHTPWYLELFPFILLGYVGGIUMAFPIRANIMCRRKSKTFKGYPLEV 404
Db 301 SRLVFEYEHTPWYLELFPFILLGYVGGIUMAFPIRANIMCRRKSKTFKGYPLEV 360
Oy 405 IIVAVTAIVAFPPYRPLNLSLKELEFPTDCCPLESSLCDYRNDNMASKITVDIDRP 464
Db 361 IIVAVTAIVAFPPYRPLNLSLKELEFPTDCCPLESSLCDYRNDNMASKITVDIDRP 420
Oy 465 AGIGVSAIMQALALJFKIIMVFTGKIVPSGLFIPSAIGAIGVIAVEOLAYY 524
Db 421 AGVGVYAMQALALJFKIIVITJTEGSMKIPSGLEIPSMAGVAGIAGVIAVEOLAYY 480
Oy 525 HHMFIFKEMCEVADCTTGLYAMVGAACLGTVTRMVSUVIYVEELTNGLEYIYPLM 584
Db 481 HHMFIFKEMCEVADCTTGLYAMVGAACLGTVTRMVSUVIYVEELTNGLEYIYPLM 540
Oy 585 AAVMTSKWVGDAFGREGIYEAHIRLNGYPPILDAAEEFTHTTLADVMRPRNDPPLAVLT 644
Db 541 AAVMTSKWVGDAFGREGIYEAHIRLNGYPPILDAAEEFTHTTLADVMRPRNDPPLAVLT 600
Oy 645 QDNMTVDIEMNINETSNGFPVIMSKSQRSLVGPALPRDLTIAESARKROEGIVSSR 704
Db 601 QDNMTVDIEMNINETSNGFPVIMSKSQRSLVGPALPRDLTIAESARKROEGIVSSR 660
Oy 705 VCFQAHPPSLPAESPRLKLSILDMSPFTVTDHTPMEIYVDFEKLGLRQCLVTHNGRL 764
Db 661 MYTEEPPELPANSPHPLKRLRIINLSPTVTDHTPMEIYVDFEKLGLRQCLVTHNGRL 720
Oy 765 LGIITKKDILRHMAOTANODPASTIMFN 791
Db 721 LGIITKKDILRHMAOTANODPASTIMFN 747

RESULT 7
CLC4_MOUSE
ID CLC4_MOUSE STANDARD: PRT: 747 AA.
AC 061418;
DT 15-JUL-1998 (Rel. 36, Created)

```

DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Chloride channel protein 4 (CLIC4).
GN	CLIC4 OR CLIC4-2 OR CLIC4.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Retina;
RX	MEDLINE=95400329; PubMed=7670496;
RA	Ruygari E.I., Adler D.A., Borsani G., Tsuchiya K., Franco B.,
RA	Hauge X., Distchev C., Chapman V., Ballabio A.;
RT	"Different chromosomal localization of the Clcn4 gene in Mus spretus
RT	and C57BL/6J mice".
RL	Nat. Genet. 10:466-471(1995).
CC	-I- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC	SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC	MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC	TRANSEPITHELIAL TRANSPORT.
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-I- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC	-I- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC	-----
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CC	-----
DR	EMBL; Z49916; CAA90150.1; -.
DR	MGI; MGI:104571; Clcn4-2.
DR	InterPro; IPR000644; CBS_domain.
DR	InterPro; IPR001807; Cl-channel_volt.
DR	Pfam; PF00571; CBS; 2.
DR	Pfam; PF00654; voltage_CLC; 1.
DR	PRINTS; PR00762; CLCHANNEL.
DR	SMART; SM00116; CBS; 2.
KW	ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW	CBS domain; Repeat.
FT	TRANSMEM 55 75 POTENTIAL.
FT	TRANSMEM 135 155 POTENTIAL.
FT	TRANSMEM 189 209 POTENTIAL.
FT	TRANSMEM 246 266 POTENTIAL.
FT	TRANSMEM 317 337 POTENTIAL.
FT	TRANSMEM 352 372 POTENTIAL.
FT	TRANSMEM 429 449 POTENTIAL.
FT	TRANSMEM 454 474 POTENTIAL.
FT	TRANSMEM 495 515 POTENTIAL.
FT	TRANSMEM 522 542 POTENTIAL.
FT	DOMAIN 586 646 POTENTIAL.
FT	DOMAIN 684 734 CBS 1.
SQ	SEQUENCE 747 AA; 83974 MW; B54866A1B0721144 CRC64;

[illegible]

QY	225	IIIRGLGWTLMIKTIITVLIVASGSLGREGPLVHAACCGNIFSVLPFKYSTNEAKR	284
Db	181	IIIRGLGWTLTIKTVILVIVLVSSGLSGKRGPLVHAACCGNIFSVLSFKYSNEKKR	240
QY	285	EVLASASAGSVAFGAPIGGVLSLEEVSYYPFLKTLMSFFAALAAEFLRSINFGN	344
Db	241	EVLASAAAAGSVAFGARIGGVLSLEEVSYYPFLKTLMSFFAALAAEFLRSINFGN	300
QY	345	SRVLVEYVEYHTPMYLFELPPILLGVFGGLMGAFETRANIAMCRKKSTKFGKYPVLEV	404
Db	301	SRVLVEYVEYHTPMYLMELPPILLGVFGGLMGTLFTRCNIAMCRKKTRILGRYPVLEV	360
QY	405	IIVAAITVIAFPNRYPLNLSLTIKELFTDCGLLESSLCDYRNDMNNAKIYDDIPDR	464
Db	361	IAAVAVTAIVAYPNIDYTRQSTSELSIELFNCGALLESSQCDYRNDNMTRPVDDIPDR	420
QY	465	AGIGVYSAINWLCALIFKIMTVEFTGIKVPSGLFIPSMNIGAIAIRIGIAVEQLAY	524
Db	421	AGVGYTATMQLALALAYKIVYITFTFGMKIRPSGLFIPSMNAGMAARMVGIGVEQLAYH	480
QY	525	IHHDFIFKEWCVEGADCIITPGLYAMVGAACLGCVTRNTYSLVIVFELTGLEGLEYVPLM	584
Db	481	IHHDMTIFERNMCRPGADCYTPGLYAMVGAACLGCVTRMTYSIVIVIMFELTGLEGLEYVPLM	540
QY	585	AAVMYSKVVGAFCFEGEGIEYEAHILNGPFLDAAKEEPTHTTIADYVRRPRNDPLAVLT	644
Db	541	AAAVTSKVVAAAFGEGEGIEYEAHILNGPFLDVADETHRLTADVVRPREDEPSVLT	600
QY	645	QDNMTVDDIEMNNIETSYNGFPMYSKESQRLVGFALRRDLTIAIESARKKOEIGVSSR	704
Db	601	QDSMTVEVELLIKETDNGFPVLVSRDSEKILGFQARREILAIKNAAROREIYVNSI	660
QY	705	VCFAPHTSPAESRPLKLSILDMSPFTVTDHTPMEIIVDIFRKLGLRQCLVTHNGRL	764
Db	661	MYFTEEPPELTPANSBHLKTRIRINLSPEYTVTDHTPMEIVDIFRKLGLRQCLVTRSGRL	720
QY	765	LGITTKRIDLRHMAOTANODPASIMFN	791
Db	721	LGITTKRIDLRHMAOMANODESIMFN	747

RESULT: 8			
CLIC5_HUMAN	STANDARD;	PRT;	746 AA.
ID	CLIC5_HUMAN		
AC	P51795.		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Chloride channel protein 5 (CLC-5).		
GN	CLIC5 OR CLIC2.		
OS	Homo sapiens (Human).		
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	MEDLINE=66121370; PubMed=8575751.		
RA	Fisher S.E., van Bakel I., Lloyd S.E., Pearce S.H.S.,		
RT	Thakker R.V., Craig I.W.;		
RT	"Cloning and characterization of CLIC5, the human kidney chloride		
RT	channel gene implicated in Dent disease (an X-linked hereditary		
RT	nephrolithiasis).";		
RL	Genomics 29:598-606(1995).		
RN	[2]		
RP	SEQUENCE OF 487-746 FROM N.A.		
RC	TISSUE=Kidney;		
RA	MEDLINE=95179126; PubMed=7874126;		
RA	Fisher S., Black G.C.M., Lloyd S.E., Hatchwell E., Wrong O.,		
RT	Thakker R.V., Craig I.W.;		
RT	"Isolation and partial characterization of a chloride channel gene		
RT	which is expressed in kidney and is a candidate for Dent's disease		
RT	(an X-linked hereditary nephrolithiasis).";		

RL Hum. Mol. Genet. 3:2053-2059(1994).
RN [3]
RP TISSUE SPECIFICITY.
RC TISSUE-Vascular smooth muscle, and Aortic endothelium;
RX MEDLINE=99222497; PubMed=10198195;
RA Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,
RA Schutte B.C.;
RT "Expression of CLCN voltage-gated chloride channel genes in human
RT blood vessels";
RL J. Mol. Cell. Cardiol. 31:657-666(1999).
RN [4]
RP VARIANTS NPHL ARG-200; LEU-244; GLU-506 AND PRO-520.
RX MEDLINE=96158876; PubMed=8559248;
RA Lloyd S.E., Pearce S.H.S., Fisher S.E., Steinmeyer K., Schwappach B.,
RA Schelman S.J., Harding B., Bolino A., Devoto M., Gooder P.,
RA Riggden S.P.A., Wrong O., Jentsch T.J., Craig I.W., Thakker R.V.;
RT "A common molecular basis for three inherited kidney stone diseases";
RL Nature 379:445-449(1996).
RN [5]
RP VARIANTS NPHL.
RX MEDLINE=97402204; PubMed=9259268;
RA Lloyd S.E., Guenther W., Pearce S.H.S., Thomson A., Bianchi M.L.,
RA Bosio M., Craig I.W., Fisher S.E., Schelman S.J., Wrong O.,
RA Jentsch T.J., Thakker R.V.;
RT "Characterisation of renal chloride channel, CLCN5, mutations in
RT hypercalcaemic nephrolithiasis (kidney stones) disorders";
RL Hum. Mol. Genet. 6:1233-1239(1997).
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN RENAL
CC TUBULAR FUNCTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: KIDNEY. MODERATELY EXPRESSED IN AORTIC
CC VASCULAR SMOOTH MUSCLE AND ENDOTHELIAL CELLS, AND AT A SLIGHTLY
CC HIGHER LEVEL IN THE CORONARY VASCULAR SMOOTH MUSCLE.
CC -1- DISEASE: DEFECTS IN CLCN5 ARE THE CAUSE OF FOUR DISORDERS OF
CC HEREDITARY HYPERCALCAEMIC NEPHROLITHIASIS (KIDNEY STONES), THAT
CC HAVE BEEN REFERRED TO AS DENT'S DISEASE (DD), X-LINKED RECESSIVE
CC NEPHROLITHIASIS (XNL), X-LINKED RECESSIVE HYPOPHOSPHATEMIC
CC RICKETS (XLRH) AND IDIOPATHIC LOW MOLECULAR WEIGHT PROTEINURIA OF
CC JAPANESE CHILDREN (JILP). ALL FOUR DISEASES REPRESENT RENAL
CC TUBULAR DISORDERS THEY ARE CHARACTERIZED BY LOW MOLECULAR WEIGHT
CC PROTEINURIA, HYPERCALCAEMIA, NEPHROCALCINOSIS, NEPHROLITHIASIS
CC (KIDNEY STONES) AND RENAL FAILURE. DD IS A FORM OF FANCONI
CC SYNDROME (ALSO KNOWN AS X-LINKED RECESSIVE NEPHROLITHIASIS TYPE 2
CC (NPHL2)).
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X91906; CAA63000.1; -;
DR EMBL: X81836; CAA57430.1; -;
DR Genew: HGNC:2023; CLCN5.
DR MIM: 300009; -;
DR MIM: 310468; -;
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; CL-channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; Voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain; Repeat; Disease mutation.
FT TRANSMEM 55 75
FT TRANSMEM 75

FT TRANSMEM 133 153 POTENTIAL.
FT TRANSMEM 189 209 POTENTIAL.
FT TRANSMEM 246 266 POTENTIAL.
FT TRANSMEM 317 337 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 428 448 POTENTIAL.
FT TRANSMEM 453 473 POTENTIAL.
FT TRANSMEM 494 514 POTENTIAL.
FT TRANSMEM 521 541 POTENTIAL.
FT DOMAIN 585 645 CBS 1.
FT DOMAIN 682 733 CBS 2.
FT DOMAIN 730 800 CBS 3.
FT VARIANT 57 57 R -> RH (IN DD).
FT VARIANT 200 200 /FTID=VAR_001615.
FT VARIANT 200 200 G -> V (IN DD).
FT VARIANT 244 244 L -> R (IN NPHL2).
FT VARIANT 280 280 S -> L (IN NPHL3).
FT VARIANT 506 506 R -> P (IN JILP).
FT VARIANT 512 512 /FTID=VAR_001619.
FT VARIANT 520 520 G -> E (IN NPHL1).
FT VARIANT 527 527 /FTID=VAR_001620.
FT VARIANT 527 527 G -> R (IN DD). ABOLISHES THE CHLORIDE
FT VARIANT 527 527 CURRENTS).
FT VARIANT 520 520 S -> P (IN NPHL2).
FT VARIANT 527 527 /FTID=VAR_001622.
FT VARIANT 527 527 E -> D (IN DD). ABOLISHES THE CHLORIDE
FT VARIANT 527 527 CURRENTS AND TOTAL LOSS OF FUNCTION).
FT VARIANT 527 527 /FTID=VAR_001623.
SQ SEQUENCE 746 AA; 83146 MW; EP9135BBA40C85D8 CRC64;

Query Match 75.2%; Score 3139.5; DB 1; Length 746;
Best Local Similarity 76.7%; Pred. No. 5.4e-217;
Matches 573; Conservative 85; Mismatches 88; Indels 1; Gaps 1;

45 LDLDDEPIPGVTDDEFTIDMVEREKDRERHRRINSKKESWEMTSLYDAMSGWLV 104
1 MDLFEEPIPGVTDDEFTIDMVEREKSDRRHREITKKSSESTWALHVSADAFSGWLV 60
105 VTGLGASGALGLIDIAADMWTDKREGICLSALYNNHCCGWSNETTPEEROKCPWK 164
61 MLTCLGSLGSLAGLIDISAHMMWTDKREGICGEMFNHCCGWSNETTPEEROKCPWK 120
165 TWAEITGQAGPSGYINMYIMFALSFALVSLVKVAPYACGSGIPEITILSGF 224
121 SMSQILISTDGAFAFYIVNYFMVLMALFALVSLVKVAPYACGSGIPEITILSGF 180
225 IIRGYLGKMTLIRITLVLAVASGLSLGKRGPLVHVACCGNIFSYLFPKYSTNEAKR 284
181 IIRGYLGKMTLIRITLVLAVASGLSLGKRGPLVHVACCGNIFSYLFPKYSTNEAKR 240
285 EVLSAASAGVAVPAGIGVLFSEVSYFFPKLTMRSEFALVAAPVLRISINPEGN 344
241 EVLSAASAGVAVPAGIGVLFSEVSYFFPKLTMRSEFALVAAPVLRISINPEGN 300
345 SRLVLFVEYHTPWLPELPETILGVEGLMGAFITRANTAMORRRKSTFGYRVLEV 404
301 SRLVLFVEYHTPWLPELPETILGVEGLMGAFITRANTAMORRRKSTFGYRVLEV 360
405 IIVAITAVIAFPNRYRLNTSELIRKLFDDCGPLLESSSLCDYRNDMAKSTVDIDPRP 464
361 LVVTAITAILAFPNRYRMTSELISLFCNCGLLDSKLCDEYRNTSKR-GGELDRP 419
465 AGIGVYSATWOLCLALFKITMVTFTGKIKVPSGLFLPSMAIGALAGIAGVIAEQLAY 524
420 AGVGVYSAMWOLCLALFKITMVTFTGKIKVPSGLFLPSMAIGALAGIAGVIAEQLAY 479
525 HHDFIRKEWCEVADCTTGLVAMVGAACIGVMTVTSVLYIVETLGGLEYIYPLM 584
480 HOEMTIVENSWSGADCTTGLVAMVGAACIGVMTVTSVLYIVETLGGLEYIYPLM 539

QY 585 AAMTSMKWDADAGRGCIYEAHRLNGYPLDLAKEEFTHTTLADYWRPRRNPPLAVLT 644
 DB 540 AAMTSMKWDADAGRGCIYEAHRLNGYPLDLAKEEFTHTTLADYWRPRRNPPLAVLT 599
 QY 645 QDMVTVDIENMINETSYNGCPYVMSKESORLGFALRDLTALIESARKKOGVGSRR 704
 DB 600 QDMVTVDIENMINETSYNGCPYVMSKESORLGFALRDLTALIESARKKOGVGSRR 659
 QY 705 VCEAQTSPSPASPRPLKRLSLDMSPTVTDHTPMEIYVDFRKLGLRQCLVTHNGRL 764
 DB 660 IYFTEHSPPLPYTPPTPLKRLNLDLSPFTVDTLPMELIYVDFRKLGLRQCLVTHNGRL 719
 QY 765 LGITTKDLIRHMAQTANODPASIMEN 791
 DB 720 LGITTKDLIRHMAQTANODPASIMEN 746

RESULT 9
 CLC5_RAT
 ID CLC5_RAT STANDARD: PRT: 746 AA.
 AC P51796; P70642;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chloride channel protein 5 (CLC-5).
 GN CLCN5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96125100; PubMed=8537381;
 RA Steimeyer K., Schwappach B., Bens M., Vandewalle A., Jentsch T.J.;
 RT "Cloning and functional expression of rat CLC-5, a chloride channel
 related to kidney disease.";
 RL J. Biol. Chem. 270:31172-31177(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96215316; PubMed=8626585;
 RA Sakamoto H., Kawasaki M., Uchida S., Sasaki S., Marumo F.;
 RT "Identification of a new outwardly rectifying Cl⁻ channel that
 belongs to a subfamily of the CLC Cl⁻ channels.";
 RL J. Biol. Chem. 271:10210-10216(1996).
 CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
 SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
 MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
 TUBULAR FUNCTION. MAY PLAY AN IMPORTANT ROLE IN RENAL
 TRANSEPITHELIAL TRANSPORT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: KIDNEY-SPECIFIC.
 CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 or send an email to license@sib-sib.ch).
 CC EMBL: Z56277; CAA91216.1; -
 DR EMBL: D50497; BA09091.1; -
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR01807; Cl-channel_volt.
 DR Pfam: PF00571; CBS_2.
 DR Pfam: PF00654; voltage_CLC_1.
 DR PRINTS: PR00762; CLCHANNEL.
 DR SMART: SM00116; CBS_2.
 KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;

KW CBS domain; Repeat.
 FT TRANSMEM 55 75 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.
 FT TRANSMEM 189 209 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 317 337 POTENTIAL.
 FT TRANSMEM 352 372 POTENTIAL.
 FT TRANSMEM 428 448 POTENTIAL.
 FT TRANSMEM 453 473 POTENTIAL.
 FT TRANSMEM 494 514 POTENTIAL.
 FT TRANSMEM 521 541 POTENTIAL.
 FT DOMAIN 585 614 CBS 1.
 FT DOMAIN 682 733 CBS 2.
 FT CONFLICT 315 315 H -> Y (IN REF. 2).
 SQ SEQUENCE 746 AA; 83067 MW; 5F17D45F397003CE CRC64;

Query Match 75.18; Score 3138.5; DB 1; Length 746;
 Best Local Similarity 76.68; Pred. No. 6,3e-217;
 Matches 572; Conservative 86; Mismatches 88; Indels 1; Gaps 1;

QY 45 LDLDLPEIPGVGYDDPHTIDWVREKCKDREHRRIRNSKKESAMETKSLYDAMSGMLV 104
 DB 1 MDLLEPIRGVGYDDPHTIDWVREKCKDREHRRIRNSKKESAMETKSLYDAMSGMLV 60
 QY 105 VTLTGLASGALGLIDIAADWMTDLKEGICLSALWYNEHOCWGSNETTPEERDKCPQWK 164
 DB 61 MLTIGLGSGLAGLIDISAHMMTDLKEGICIGTGFWEHHEHCWNSHVPFEDRDKCEWN 120
 QY 165 TMAELIIGAGEGSGYIMNIMYFALNAPLAVSLYKFAFYACGSGIPETKLTISGF 224
 DB 121 SMSOLITSDOGAFAYIVNFMVLAALFAFLAVSLYKFAFYACGSGIPETKLTISGF 180
 QY 225 IIRGYGKMTLKITTLVLAVASGLKEGPLVHVACCCGTFSPKYSTNEAKR 284
 DB 181 IIRGYGKMTLKITTLVLAVASGLKEGPLVHVACCCGTFSPKYSTNEAKR 240
 QY 285 EYLSAASAGSVAFGAPIGCVLFSLSEVSYRPLKLTMSRFAALVAFVLSINPFGN 344
 DB 241 EYLSAASAGSVAFGAPIGCVLFSLSEVSYRPLKLTMSRFAALVAFVLSINPFGN 300
 QY 345 SRLVLYVEHTPWYLFELPFLILGVFGMLGAFIRAIAMCRKRKSPKRYPLEV 404
 DB 301 SRLVLYVEHTPWYLFELPFLILGVFGMLGAFIRAIAMCRKRKSPKRYPLEV 360
 QY 405 IYVAATVAVFPNPTRLTSELKELFTDCGPLSSLCDVRNRMASKIYDDIPDR 464
 DB 361 IYVAATVAVFPNPTRLTSELKELFTDCGPLSSLCDVRNRMASKIYDDIPDR 419
 QY 465 AGIGVSAIWQLCLAFIKIIMTVFTFGIRKVPISGLFTPSMAIGAGRIAGVIAVEOLAVY 524
 DB 420 AGIGVSAIWQLCLAFIKIIMTVFTFGIRKVPISGLFTPSMAIGAGRIAGVIAVEOLAVY 479
 QY 525 HHDMFTFKKECEVAGACITPGILAVWGAACLOGVTRMYSLVYVIFELTGLGLEYVPLM 584
 DB 480 HHDMFTFKKECEVAGACITPGILAVWGAACLOGVTRMYSLVYVIFELTGLGLEYVPLM 539
 QY 585 AAMTSMKWDADAGRGCIYEAHRLNGYPLDLAKEEFTHTTLADYWRPRRNPPLAVLT 644
 DB 540 AAMTSMKWDADAGRGCIYEAHRLNGYPLDLAKEEFTHTTLADYWRPRRNPPLAVLT 599
 QY 645 QDMVTVDIENMINETSYNGCPYVMSKESORLGFALRDLTALIESARKKOGVGSRR 704
 DB 600 QDMVTVDIENMINETSYNGCPYVMSKESORLGFALRDLTALIESARKKOGVGSRR 659
 QY 705 VCEAQTSPSPASPRPLKRLSLDMSPTVTDHTPMEIYVDFRKLGLRQCLVTHNGRL 764
 DB 660 IYFTEHSPPLPYTPPTPLKRLNLDLSPFTVDTLPMELIYVDFRKLGLRQCLVTHNGRL 719
 QY 765 LGITTKDLIRHMAQTANODPASIMEN 791
 DB 720 LGITTKDLIRHMAQTANODPASIMEN 746


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RX MEDLINE=95018225; PubMed=7932715;
RA Huang M.-E., Chuat J.-C., Galibert F.;
RT "A voltage-gated chloride channel in the yeast Saccharomyces
RT cerevisiae."
RT J. Mol. Biol. 242:595-598(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RX MEDLINE=95397595; PubMed=7668047;
RA Huang M.-E., Chuat J.-C., Galibert F.;
RT "Analysis of a 42.5 kb DNA sequence of chromosome X reveals three
RT tRNA genes and 14 new open reading frames including a gene most
RT probably belonging to the family of ubiquitin-protein ligases."
RT least 11:775-781(1995).
RL
CC -i- FUNCTION: TRANSPORT PROTEIN INVOLVED IN INTRACELLULAR IRON
CC METABOLISM DURING GROWTH ON FERMENTABLE AND NON FERMENTABLE CARBON
CC SOURCES. POTENTIAL VOLTAGE-GATED CHLORIDE CHANNEL.
CC -i- SUBUNIT: HOMOTETRAMER (PROBABLE).
CC -i- SUBCELLULAR LOCATION: Integral membrane protein.
CC -i- SIMILARITY: TO E. COLI YAD0 AND TO CHLORIDE CHANNEL PROTEINS.
CC -i- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL: Z23117; CAA80663.1; -
DR EMBL: L29347; AAA53389.1; -
DR EMBL: Z49540; CAA89387.1; -
DR EMBL: L36344; AAA8741.1; -
DR PIR: S39904; S39904.
DR SGD: S0003801; GEF1.
DR InterPro: IPR000644; CBS domain.
DR InterPro: IPR001807; Cl-channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; Voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain; Repeat.
FT TRANSMEM 76 POTENTIAL.
FT TRANSMEM 155 175 POTENTIAL.
FT TRANSMEM 178 198 POTENTIAL.
FT TRANSMEM 204 224 POTENTIAL.
FT TRANSMEM 265 285 POTENTIAL.
FT TRANSMEM 337 357 POTENTIAL.
FT TRANSMEM 437 457 POTENTIAL.
FT TRANSMEM 489 509 POTENTIAL.
FT TRANSMEM 521 541 POTENTIAL.
FT TRANSMEM 589 652 CBS 1.
FT DOMAIN 686 738 CBS 2.
FT CONFLICT 13 R->G (IN REF. 2).
FT CONFLICT 207 L->F (IN REF. 2).
FT CONFLICT 257 T->S (IN REF. 2).
FT CONFLICT 262 L->I (IN REF. 2).
FT CONFLICT 497 I->T (IN REF. 2).
SO SEQUENCE 779 AA; 87682 MW; 56D86B3DE2FE25C CRC64;

Query Match 23.9%; Score 996.5; DB 1; Length 779;
Best Local Similarity 32.8%; Pred. No. 1,1e-63;
Matches 254; Conservative 151; Mismatches 253; Indels 117; Gaps 25;

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QY 155 EERDKCPQ---WKTAEITIGAECPGYIMNYIMINAFSLAVLSVAFYACG 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 137 ROEFCEAGGLMIAMK-----GHVSPIIFMLSVLFALISTLVKXVAMAG 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 212 SGIPKEITLISGF-IIRGLGKWTLMKITITLVLAASGLISGKEPLVHVAOCNNIFS 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 186 SGISEIKVWVSFEYINKEFGLTLTVIKSVLPLAISLSGKESGSPVHYATCC----- 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 271 YLFPK-----YSTNEAKKREVLSAASAGVAFAPIGVLFSTEEV---SYFPLK 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 242 YLTTLKRLDITLYSI---QYEYLTAAAGACVAAFAPICGVLFGLFEISANFNSS 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 321 TLWRSFALVAEYVLRISINPGNSRLVFEYEHYTPWYLFELPEPILLVGFGMGAF 380
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 298 TLWKSYYVALVATITLKYIDPFRNGVILFNVTYDRMKVQOEIPFIALGIFGLGKYI 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 381 ITANIAMCRKRSKTRKGPVLEVIIVAAITVAIPNRYTRINSELKELTDCGPLE 440
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 358 SKWNINFIHFRK-WYSSMPQVFLVATVLTALISTFNEFLKIDMTESGILFHECVKND 416
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 441 SSS-----LCDYRNDNMASKIVDDIPDPAGIGVYSAIWQLALIKITMTVFTGIV 495
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 417 NNTSPSHRLCGQDENHAEFL-----KIFSLCEATYIRALLVVSYGAV 463
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 496 PGGLFIPSAIGALAGRIAGVLAEOLAYHHDMFTKWECEVADCTPGLYAMGAAC 555
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 464 PAGIFPMAVAGTAEGRASVLVER-----FI-----SGPSVIIGAVAFILGAAT 509
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 556 LGVTRMTYSIVVPELVFGLGLEYIVLMAAVMTSKWVDAG-REGIYEAHRLMGYF 614
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 510 LSGITNLTLVVVIMELGAFMYIIPLMIVVATIRILISTSGISGIDOMIMVGPY 569
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 615 L-----DAKEEFTHTLAADVMPRRNDPLAVLTQDNMTVDIENMI---NETSYNCP 666
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 570 LDEQDEEEEFLEKXTAQIMSK-----LITINFTIYLSLESLLYSASEYSVHGPP 624
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 667 VIMSK-----SRLVGFALRDLT--IAIESARKQEGIVGSRVCEAQTPLPAESR 720
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 625 ITRKDEKFEKERKICGYVLRHLASKIMQSVNSTR---AQTLVYFNKSNEL-CHREN 680
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 721 PLKSLIDMSPTFYDTHPMELVDFRKLGLRQCLVTHNRLGLITKKDILR 775
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 681 CIGFKDINMSPTSVKAVPTLLFRFKELGCKTIIVEESGILGLVYAKDILR 735
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
CLC7_MOUSE STANDARD; PRT; 803 AA.
AC 070496:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 7 (CLC-7).
GN CLCN7 OR CLC7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21124827; PubMed=11207362;
RA Kornak U., Kasper D., Bosl M.R., Kaiser E., Schweizer M., Schulz A.,
RA Friedrich W., Delling G., Jentsch T.J.;
RT "Loss of the CLC-7 chloride channel leads to osteopetrosis in mice
RT and man."
RL Cell 104:205-215(2001).
CC -i- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT.
CC -i- SUBCELLULAR LOCATION: Integral membrane protein.
CC -i- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.

```

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CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF063101; AAC18832.1; JOINED.
DR EMBL: AF063098; AAC18832.1; JOINED.
DR EMBL: AF063099; AAC18832.1; JOINED.
DR EMBL: AF063100; AAC18832.1; JOINED.
DR MCD: MGI:1347048; C1cn7.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl-channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain; Repeat.
FT TRANSMEM 126 146 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 222 242 POTENTIAL.
FT TRANSMEM 290 310 POTENTIAL.
FT TRANSMEM 373 393 POTENTIAL.
FT TRANSMEM 410 430 POTENTIAL.
FT TRANSMEM 493 513 POTENTIAL.
FT TRANSMEM 516 536 POTENTIAL.
FT TRANSMEM 579 599 POTENTIAL.
FT DOMAIN 627 674 CBS 1.
FT DOMAIN 737 781 CBS 2.
SQ SEQUENCE 803 AA; 88712 MW; A7D6DA5791DAA48C CRC64;

Query Match 18.08; Score 751, DB 1; Length 803;
Best Local Similarity 29.14; Pred. No. 4.2e-46;
Matches 249; Conservative 139; Mismatches 270; Indels 198; Gaps 38;

26 RGTHTYMTNGSINSSTHLLDDEPIRGVGYD-----DPIHTDWR-EKCK 72
45 RQSHSALEFRIGOMNNVLEDELDEPDPHTPEKIPHNKLLSLKYESLDYDENSEQL 104
73 DREHRRIRNSKKESAMEMKSLYDAMSGMLVLTGLASGALAGLDIDAMWTDEKEG 132
105 FLEBERIRIN---HTAFRTVEI---KRWYICALIGLGLVACFDIYVENAGLKYR 155
133 ICLSAIWNHEQCCWGSNETFEERDKCPQKTYAELLIGQAEGPSYIMNYITFWA- 191
156 VI-----KNDIKFTEK-----GGLSFSL-----LMAT 179
192 LSPFAFLAVS--LVKVPAYAGSGIPEKTIILSGFIIRGYLGKWTLMIKITTLVAVSG 249
180 LNSAFVLVGSYIAVFIIPVAGSGIPIKCFPLNCKIPHYVRLTKVIKSGVLSVVG 239
250 LSLQKESPLVHVACCNIFS-----YLFPKYSTNAKRREVLNAAAGV 295
240 LAVGKEGPMIH---SGSVIAAGISQGRSTSLKRDPKIFEFRRDTEKRPVSAAGV 295
296 SVAFGAIIGVLSLEVSYTFPLKTLMRSEFALVAFLVRSINP--GN-----SRL 347
296 SAAGFAGVGGLFLLEGASFMNQFLTWRIFFASMTFTLNFELSLHYGMMDLSSPGL 355
348 VLF--YVEYHTPWLEFLEFPIILGVFGGLMGAFIIRANIAMCRRRSTKFG-KY----- 399
356 INFERPSEKMAVTHIEIPVFIANGVGLGAVFALNLY-WL-----TMRIRYIHRPC 409
400 -PYLEVIYVAITVAIFPVPYRLNTSELIKELFTDCGLESSL-----C---DYL 448
410 LQVTEANLVAAVTAFTAVFLYSS-----RDCQPLQSSSMKYPIQLFCADEY- 457
449 NDMAAS-----KIYDIDPRAGIGVSAIMQCLALIFKIIIMVFTFGIKVPSGLFI 501

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DB 458 NSMAAFENFTEPKSVSLFHDPP---GSYNPMILGFTLYV-FELACWTFGLVSAAGVI 513
QY 502 PSMALGACAGIVAINVQALAYHHDFIKREKCEVADCTPGLVWMAAGACLGVT 561
DB 514 PSLIIGAWGRLFSISLYLT-----GAIWAD--PKYALDKGAADLGSIIVR 559
QY 562 MTSLVVIVELTNGLEYIYPLMAAVMTSKWGDAPFREGIEYEAHLINLNGPFLDAKEEF 621
DB 560 MTLSLVYIMMETSNTVNYGPFIMLVMTAKIVGVF-IEGLYDHIIDOLGSPFLHMAVP 618
QY 622 T-HTTLADVRRPRRNDPLAVLTQDMVTYDDIENMINET--SYNGFPVIM---SKSOR 675
DB 619 TSHSLTAREWV---STPYCLRR-REKVGIIYVDLSDTASNHNNGPVEDVDQTPAR 672
QY 676 LVGFALRDLTIAESARKKOEIGVSSRCFPAQHT-----PSLPA----- 716
DB 673 LOGILRSQLVLL-----KIKVFEKSNGLVDRRLKDFRDVAYRPPPIISHSQD 727
QY 717 ESPRPLKRLSIIDSPFTVTDHPMEIYVDIFRKLGRQCLVTHN-GRLLGIITRKDLR 775
DB 728 ERECTMDLSEFMNPSPTYVQEASLPVFKLFRALGLRHLVYVDNHNQVGLVTRKOLAR 787
QY 776 H-----MAQT 780
DB 788 YRLGKGGLLELSLAOT 803

RESULT 13
CLC7_RAT STANDARD; PRT; 803 AA.
ID CLC7_RAT
AC P51799;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 7 (CLC-7).
GN CLCN7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=96130311; Pubmed=8543009;
RX Brandt S., Jentsch T.J.;
RT "CLC-6 and CLC-7 are two novel broadly expressed members of the CLC
RT chloride channel family";
RL FEBS Lett. 377:15-20(1995).
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, TESTIS, MUSCLE AND KIDNEY.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z67744; CA91557.1; -.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl-channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.

```

KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
 KW CBS domain; Repeat.
 FT TRANSMEM 126 POTENTIAL.
 FT TRANSMEM 175 POTENTIAL.
 FT TRANSMEM 222 POTENTIAL.
 FT TRANSMEM 290 POTENTIAL.
 FT TRANSMEM 373 POTENTIAL.
 FT TRANSMEM 410 POTENTIAL.
 FT TRANSMEM 493 POTENTIAL.
 FT TRANSMEM 513 POTENTIAL.
 FT TRANSMEM 579 POTENTIAL.
 FT TRANSMEM 599 POTENTIAL.
 FT TRANSMEM 627 CBS 1.
 FT TRANSMEM 674 CBS 2.
 FT TRANSMEM 737 CBS 2.
 FT TRANSMEM 781 CBS 2.
 FT TRANSMEM 803 AA: A7D6AA3D21DA6EED CRC64;
 SQ SEQUENCE

Query Match 18.0%; Score 751; DB 1; Length 803;
 Best Local Similarity 29.1%; Pred. No. 4.2e-46;
 Matches 249; Conservative 139; Mismatches 270; Indels 198; Gaps 38;

26 RGHHTMTGSGINSSTHLLDLEPIPGVTD-----DFTIDVR-EKCK 72
 45 RQSHSLFRTGQNNVLELDELDPVDPHPFKRIPNEKLSLKYESLDVDSNGL 104
 73 DRRHRIRSKKESAMETKSLYDAMSGVLVYTLGLAGLALIDIAADMTDLKGG 132
 105 FLEERRRIN---HTAFRTVEI---KRWVICALIGITGLVACFIDIVENMLGLKYR 155
 133 ICSALMYNHQCCWGSNTTEFEERDKCPQWKTMALLIGQAGPSYIMNYMTYFNA- 191
 156 VT-----KDNIDKFTKK-----GGLSFSL-----LLMAT 179
 192 LSFAPLAVS--LVKVPAPACSGIPEIKTILSGFIIRGLGKWTMTITFLVAVASG 249
 180 LNSAFVLVGSVIAFLEFPAAAGSGIPQIKCPLNGVKIRPHVRLKTIIVISGILSVGG 239
 250 LSLGKGPLVHVACCCGNIFS-----YLPKYSTNEAKKREVLSAASAGV 295
 240 LAVGKGGPMIH---SGSVIAGISQGRSTSLKRDPKIEYFRDREKDFVSAGAAAGV 295
 296 SVAFGAPIGGVLFSEEEVGYFPLKTLMSFPALVAVALVLSINF--GN-----SLU 347
 296 SAAFGAPVGVGLFSEEGSFMWQPLTMRIFPASMSTLTFLNVLISYIGNMDLSSPGL 355
 348 VLF--VVEYHTPMYLELPFLLGLVGLGAFETRANIAMCRKRSTKFG-KY----- 399
 356 INGRDSEKMAVTHIEIVFIAMGVGILGAVENALNV-WL-----IMFRIRYIHRC 409
 400 -VYLEVTIYAATVAVAFNPPTRLNTSELIKELFTDCCPLESSSL-----C---DYR 448
 410 LGVIEAMLVAAVATVAVAFVLIYS-----RDCOPLOGSSMSYPLQLFCADGEY- 457
 449 NDMNAS-----KIYDDIPDRPAGIGVSAIMQLCLALIFKTIIMVFPGIKVPSGLTI 501
 458 NSMAAFAFETPEKSVSLFHPDP--GSYNPMLGLFTLVY-FELACWYIGLIVSGAVTI 513
 502 PSMAIGALIRIGVIAVEOLAVYHDMVLFKECEVGADCIPTGLIYAMGAACAGLEGVTR 561
 514 PSLLIGAAMGRLEFGISMSYLT-----GAATWAD--PGKVALMGAAAGAGGIYR 559
 562 MIVSLVIVYFELTGLLEYVPLMAAVMTSKVGDAGFRGITYEAHIRLNGVPEPLDAKEEF 621
 560 MRLSLVIMMEATSVNTYGFPTMLVMTAKIVGDV-FIGLIDMHQLOSQVFLHMEADV 618
 622 T-HTTLAADVPRRRNDPPLAVITODNMVVDIENNINFT--SYNGFPIVM--SKESOR 675
 619 TTSISLTAAREV-----STPYTCLRR-REKVGIITVDLSITASNHNSEFVVEDVGTOPAR 672
 676 LVGFALRDLITAIESARKKQGIYSSRVCEAORT-----PSLPA----- 716
 673 LGLILRSQILIVL-----KHKVFYERSNMGLVQRRRLKDFRDVAPRRPPIQSIHVSD 727
 717 ESRRLKLSIIDMSPFYTDHTPMEITVVDIFRKGLRQCLVYHN-GRLLGITTKKDLIR 775

DB 728 ERECTMDSFNNPSPYTPQEASLPRVKLFRLALRLHVLVVDNHNQVGLVTRKDLAR 787
 QY 776 H-----MAOT 780
 DB 788 YRLGKGLEBLSLAOT 803

RESULT 14
 CLC7_HUMAN
 ID CLC7_HUMAN STANDARD; PRT; 805 AA.
 AC P51798; Q9NYX5;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chloride channel protein 7 (CLC-7).
 GN CLCN7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Rae J.L.;
 RT "Ion channels in lens epithelia."
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA TISSUE=skin;
 RC Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 RN (3)
 RP SEQUENCE OF 17-805 FROM N.A.
 RC TISSUE=brain;
 RX MEDLINE=96130311; PubMed=8543009;
 RA Brandt S., Jentsch T.J.;
 RT "CLC-6 and CLC-7 are two novel broadly expressed members of the CLC
 RT chloride channel family."
 RL FEBS Lett. 377:15-20(1995).
 RN (4)
 RP SEQUENCE OF 275-432 FROM N.A.
 RX MEDLINE=98234303; PubMed=9565675;
 RA Eggermont J.;
 RT "The exon-intron architecture of human chloride channel genes is not
 RT conserved."
 RL Biochim. Biophys. Acta 1397:156-160(1998).
 RN (5)
 RP SEQUENCE OF 744-805 FROM N.A.
 RC TISSUE=breast;
 RA Schutte B.C., Malik M.I., Fingert J., Stone E., Lamb F.S.;
 RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
 CC SEVERAL POTENTIALS INCLUDING THE REGULATION OF CELL VOLUME;
 CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
 CC TRANSEPIHELIAL TRANSPORT.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: BRAIN, TESTIS, MUSCLE AND KIDNEY.
 CC -!- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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 CC
 CC EMBL: AF224741; AAF34711.1;
 CC EMBL: BC012737; AAH12737.1;
 CC EMBL: 267743; CA91556.1;
 CC EMBL: AJ001910; CA05083.1;
 CC EMBL: U08844; AAB48550.1;
 CC Genew; HGNC:2025; CLCN7.

```

DR MIT; 602727; -.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; C1-channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; Voltage_C1C; 1.
DR PRINTS: PR00762; C1CHANNEL.
DR SMART: SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain; Repeat.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 224 244 POTENTIAL.
FT TRANSMEM 292 312 POTENTIAL.
FT TRANSMEM 375 395 POTENTIAL.
FT TRANSMEM 412 432 POTENTIAL.
FT TRANSMEM 495 515 POTENTIAL.
FT TRANSMEM 518 538 POTENTIAL.
FT TRANSMEM 581 601 POTENTIAL.
FT DOMAIN 629 674 CBS 1.
FT DOMAIN 739 783 CBS 2.
FT CONFLICT 267 267 T -> S (IN REF. 3).
FT CONFLICT 279 279 T -> L (IN REF. 3 AND 4).
SO SQUENCE 805 AA; 88679 MW; E56BC0BADADELIC695 CRC64;

Query Match 17.98; Score 748.5; DB 1; Length 805;
Best Local Similarity 29.88; Pred. No. 6.3e-46;
Matches 237; Conservative 131; Mismatches 241; Indels 185; Caps 36;

OY 75 ERHRINSKKESAMEMTKSLYDAMSGMLVYVTLGLASGALGLDIAADMVTLKSGIC 134
| ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 109 EEEERIN---HTAFRVER-----KRWICALGLIGLACTIDIVELAGLKRVT 159
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 135 LSLALYNHEDOCWMSNTEFEERDKCPQMKTWALLIQAQPSGYIMNYIMYFMA-LS 193
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 -----KGNIDKFEK-----GGLSFSL-----LLMFTLN 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 194 FAPLAVS--LYKVAAPACSGAIPETITISGFIIRGLGKWTMTITITLVAVASGLS 251
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 AAFVLSVAVAFLEPVAAGSGIPIKCNGLNGVKIPHVVRKLTIVIVSGVILSVGGLA 243
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 252 LGRGPIVHVAACCGNIES-----YLPKYSNEAKKREVLASAAGVSV 297
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 VGRGPIH-----SGYIAGISGGRSTSLKRFKIFEFRRDKEDVYSAAGAAGVSA 299
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 298 AFGAPIGVLFLEEVSYEPPLKTLMSFFAALVAALVLSINPF--GN-----SRLVL 349
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 300 AFGAPVGVLFLEEGASFMNQFLTWRFASMTFTLVNLVLTIGHNMMDLSSPGLIN 359
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 350 F--YVEHTWYLFLEPFILGVFGGLMGAFPIRANIAMCRKRSKTFG-KY-----P 400
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 360 FGREDSEKMAVTHIEIFVFIAMGVGVGLVAFNALNY-WL-----TMFRLRYTHRCLO 413
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 401 VLEVIYAATAVAIAFNPYTRLTSLIKELFTDCGPLESSSL-----C--DYRND 450
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 414 VIEVAVAAVTAIVAFVLIYSS-----RDCOPLOGGSWYPLDLCADGET-NS 461
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 451 MNAS-----KIYDDIPDRPAGIGVYSATWOLCLALIFKILMTVFTEGKIVPSGLETPS 503
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 462 MAFAFNTPEKSVSLFHDP-----GSYNPLTLGLFTLVY--FELLCWYTGTLVSGVFLPS 517
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 504 MARGALGRIVGLAVEDOLAYHHDMFLFKEMCEVAGDCITPGLYAMGAACLAGVTRMT 563
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 518 LLGGAAGRFGISLSLYL-----GAAIWD--PGKYALMGAAAOLOGIVRMT 563
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 564 VSLVIVFEELTGLGLEYIVPLAAVMTSKWYGDAFGREGIYEAHIRLNGYFLAKKEFT- 622
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 564 LSLFVIMMEATSNVTFPPLIMLVMTAKIVGVDF-IGELDMHQLQSVPLHMEAVTS 622
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 623 HTTLADVMPRRNDPLAVLTODNMVDDIENMINET--SYNGFPYIM--SKESORLV 677
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 623 HSLTAREVM---STPYTCLRRKRGV--IVDVLSTASHNNGFPVVEHADTPPARLO 676
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 678 GFALRDLTLTAIESARKKQEGIVSSRVCFRQHT-----PSLPA-----ES 718
| : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db 677 GLILRSQILVL-----KHKVVERSNGLGVQRRLRLKDFEDAYRPPPIIOSIHVSODER 731
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 719 PRPLKLSILDMSPFTYDTHDPMEIYVDIFPKLGLROCLVTHN--GRLLGITTKDILRH- 776
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 732 ECTMDLSEFMNPSPTYPQEAESLPRVFKRLFRALRLHLYVDNKNQVGLTRDLARIR 791
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 777 -----MAQT 780
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 792 LGRKGLBELSLAQT 805
| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
CLC6_HUMAN STANDARD; PRT; 869 AA.
AC P51797; P78521; O60818; O60819; O60820; O60821; Q99427; Q99428;
AC Q99429; P78520;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 6 (CLC-6).
GN CLCN6 OR KIAA0046.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=96130311; PubMed=8543009;
RA Brand S., Jentsch T.J.;
RT "CLC-6 and CLC-7 are two novel broadly expressed members of the CLC
RT chloride channel family.";
RL FEBS Lett. 377:15-20(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D), AND SEQUENCE OF 1-409 FROM
RP N.A. (ISOFORM A).
RC TISSUE=Chronic myeloid leukemia cell;
RX MEDLINE=97344267; PubMed=9224655;
RA Egermont J., Buysse G., Voets T., Tylgat J., De Smedt H.,
RA D'ocmans G., Milius B.;
RT "Alternative splicing of CLC-6 (a member of the CLC chloride-channel
RT family) transcripts generates three truncated isoforms one of which,
RT CLC-6c, is kidney-specific.";
RL Biochem. J. 325:269-276(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX PubMed=10500249;
RA Kornak U., Boesi M.R., Kubisch C.;
RT "Complete genomic structure of the CLCN6 and CLCN7 putative chloride
RT channel genes.";
RL Biochim. Biophys. Acta 1447:100-106(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RA Ohara O., Nagase T., Kikuno R., Nomura N.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 50-869 FROM N.A., AND ALTERNATIVE SPLICING.
RA Errington H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 237-869 FROM N.A. (ISOFORM A).
RC TISSUE=Bone marrow;
RX MEDLINE=96051398; PubMed=7584044;
RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
RA Seki I., Kawarabayashi Y., Ishikawa K.-T., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. II.
RT The coding sequences of 40 new genes (KIA0041-KIA0080) deduced by
RT DNA Res. 1:223-229(1994).
RN [7]
RP TISSUE SPECIFICITY.

```

RC TISSUE-Vascular smooth muscle, and Aortic endothelium;
 RX MEDLINE:99222497; PubMed=10198195;
 RA Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,
 RA Schulte B.C.;
 RT "Expression of CLCN voltage-gated chloride channel genes in human
 RT blood vessels.";
 RL J. Mol. Cell. Cardiol. 31:657-666(1999).
 CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
 CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
 CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
 CC TRANSEPITHELIAL TRANSPORT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; A/C1c-6a (shown here), B/C1c-
 CC 6b/2-A1, C/C1c-6c/D1-A1 and D/C1c-6d/D1-A2; are produced by
 CC alternative splicing.
 CC -1- TISSUE SPECIFICITY: Testis, ovary, small intestine, brain and
 CC skeletal muscle. Low level expression in aortic and coronary
 CC vascular smooth muscle cells, and aortic endothelial cells.
 CC Isoform C is only detected in kidney.
 CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC -----
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 CC -----
 DR EMBL: X83378; CAA58292.1; -
 DR EMBL: X96391; CAA65255.1; -
 DR EMBL: X99472; CAA67835.1; -
 DR EMBL: X99473; CAA67836.1; -
 DR EMBL: X99474; CAA67837.1; -
 DR EMBL: X99475; CAA67838.1; -
 DR EMBL: AF009257; AAB69287.1; -
 DR EMBL: AF009247; AAB69287.1; JOINED.
 DR EMBL: AF009248; AAB69287.1; JOINED.
 DR EMBL: AF009249; AAB69287.1; JOINED.
 DR EMBL: AF009250; AAB69287.1; JOINED.
 DR EMBL: AF009251; AAB69287.1; JOINED.
 DR EMBL: AF009252; AAB69287.1; JOINED.
 DR EMBL: AF009253; AAB69287.1; JOINED.
 DR EMBL: AF009254; AAB69287.1; JOINED.
 DR EMBL: AF009255; AAB69287.1; JOINED.
 DR EMBL: AF009256; AAB69287.1; JOINED.
 DR EMBL: AL021155; CAA15951.1; -
 DR EMBL: AL021155; CAA15952.1; -
 DR EMBL: AL021155; CAA15953.1; -
 DR EMBL: AL021155; CAA15954.1; -
 DR EMBL: D28475; BAA05836.3; -
 DR Gene: HGNC:2024; CLCN6.
 DR MIM: 602726; -
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR001807; Cl_channel_volt.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00554; voltage_CLC; 1.
 DR PRINTS: PR00762; CLCHANNEL.
 DR SMART: SM00116; CBS; 2.
 KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
 KW CBS domain; Repeat; Alternative splicing.
 FT TRANSMEM 82 102 POTENTIAL.
 FT TRANSMEM 130 150 POTENTIAL.
 FT TRANSMEM 164 204 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 334 354 POTENTIAL.
 FT TRANSMEM 375 395 POTENTIAL.
 FT TRANSMEM 462 482 POTENTIAL.
 FT TRANSMEM 511 531 POTENTIAL.
 FT DOMAIN 603 658 CBS 1.
 FT DOMAIN 805 856 CBS 2.
 FT DOMAIN 4 18 CYS-RICH.

FT VARSP LIC 237 320 DKRDVYSAAGAAAFAPAGTIGTLFSLSEGGSPFNQGIT
 FT FT KVLVFCMSATFTLNFRRSGTIOFGSMGSPQLPFLNFGFK
 FT FT CS -> YGKROERLTISRSGCMSCSPRGANRGYILOSNG
 FT FT FYLLERPAVESALLFHVCHLHPQLLPFMDSVKLGFLFAP
 FT FT WIELMRV (IN ISOFORM B).
 FT FT MISSING (IN ISOFORM B).
 FT FT CSDDKRCHEMTLGFVPMGLGGLGATPNC -> SL
 FT FT REPCVGNHRCVCGCLDGVRRMPTDVLFSNR (IN
 FT FT ISOFORM C).
 FT FT MISSING (IN ISOFORM C).
 FT FT DKRDVYSAAGAAAFAPAGTIGTLFSLSEGGSPFNQGIT
 FT FT KVLVFCMSATFTLNFRRSGTIOFGSMGSPQL -> SGCMSC
 FT FT CSFRGANRGYILOSNGFVLLERPAVESALLFHVCHLHP
 FT FT LPEFMDSVKLGFLFAPWIELMRV (IN ISOFORM D).
 FT FT MISSING (IN ISOFORM D).
 FT FT G -> E (IN REF. 5).
 FT FT CONFLICT 198 198
 FT FT SEQUENCE 869 AA: 97216 MM: E423777D9FF4328 CRC64;
 SO
 Query Match 17.4%; Score 725.5; DB 1; Length 869;
 Best local Similarity 25.3%; Pred. No. 3,1e-44;
 Matches 235; Conservative 142; Mismatches 245; Indels 307; Gaps 35;
 QY 49 DEPIPGVGYDDHTIDWREKC-----KDERHRRINSKKESAMEXTSLYD 97
 DB 40 DETLP-----RKDESDLY--DRCINDPYLEVTMDKKGRREAVK----- 80
 QY 98 AMGWLVVTLTLGLASGALGLIDIDMDMTDKEGICLSLAWNHECCMGNETFEER 157
 DB 81 ----MMVFAIGCTGLVGLVDFVRLFTOLKRGVV-----QTSEE- 119
 QY 158 DKCPQMKTWAEILLGOEFGSYIMNYITFALSAFPLAVLVKFAFACSGSIPET 217
 DB 120 --CSQ-----KGLCALSLLELLGNLTFFVFLA-SLVLIIEVVAAGSGIPEV 162
 QY 218 KTLTSGFIITIGYKTKMTKTTTLVLAASGLSGKEGPLVHVACCG----- 266
 DB 163 KCYLNGKVPYIVRLFTLLCKVGLFVSVAGLVFGVEGKPMHSGSVYAGLPQFOSISL 222
 QY 267 NIFSYLEPFRKSTDEAKKREVLASAAGVAVFAGAPIGVLFSLSESYFELPKTLMRSF 326
 DB 223 RKIQFNFP-YFRSDRDKRDVSAGAAVAAAFAPAGTIGTLFSLSEGGSPFNQGIT 281
 QY 327 FAALVAFAVLR-----SINFGNSRL--VLFYVEVHTP-----WYLFELFPITLG 370
 DB 282 FCGMSATFTLNFRRSGTIOFGSMGSPQLPGLNFGFRCSDSKCHMTMDGFFVVG 341
 QY 371 VEGGLMGAFPIFRANIAMCRKRKSTK- -GKYP-----VLEVIYAATAVIAFPNPT 421
 DB 342 VIGLLGATFN-----CLNKRRLAKYRMRVHPRKLVRLVLSLVSIVTVVVF----- 390
 QY 422 RLMTSELIKELFTDGGPLESSSLCDVRNMDNASKIYDDI----- 460
 DB 391 -----VASNVLGECCROMSSS--QIGNDSFQLOVEDVASSIKTFPCPDYNDMATLF 442
 QY 461 --PDRPAGI-----GYSAIMOLCLALFKIIMVTFEGIKVPSGLFIPSMAGIATGR 512
 DB 443 FNPQESATLQLFHQDGFSPV-TLALFVLYFLLACCTVTSVPSGLFVSLGCAAFGR 501
 QY 513 IYCIANEQLAYIHDMFIREKCEVGAADCTPGLYAVNGAACACLGVTAKTVSLVIVFE 572
 DB 502 LVANVLKSY-----IGIGHIYSGTFALIGAALGLGVVRMTISLTVLLIE 546
 QY 573 LINGLEIYVLMAYMTSKVGVDAFGEIGYEAHIRLNGVPEFLDAKEEFHTTL-AADV 631
 DB 547 STNELTYGELIVTLMAKWTGDFPNK-GTYDTHVGRGPLLEMETEVEDMKLRASDIM 605
 QY 632 RPRRNDPPLAVLTQDNMT-----VDIEENMINTSYNGFPI----- 668
 DB 606 EP-----NLTYVYPHTRIQSLVSLRTTYVHAAPVVTENRGNEKPEMKNQL 652
 QY 669 -----MSKESQRLVGF--ALRR--DLTAIESARKQD----- 697
 DB 653 ISNNIKFKKSSILTRAGEORRKSQSMKSYPSSELRNMCDEHIASEPAEKEDLLQOMLER 712


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QY 698 -----GIVGSSR-----VCEAQHTPSLPASP 719
Db 713 RYTPYPNLYPDQSPSEDWTEERFRPLTFHGLIRSQLVTLVARGCYSESQSS--ASQP 770
QY 720 R-----PLKLRSLIDM-----SPTVTDHTPMEIVVDIFRKL 751
Db 771 RLSYAEMAEADYPRYPDIHDLDTLLNPRMIVDTPYMNPSPTVSPNTHVSQVFNLFRTM 830
QY 752 GLROC-LVTNHRRLGILTKKDIIRHMAQ 779
Db 831 GLRHLPYVNAVGEIVGIITRHNLTYEFLQ 859

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Search completed: May 12, 2003, 15:03:19
 Job time : 31 secs